GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2004, 08:35:47 ; Search time 0.001 Seconds
(without alignments)
1724.344 Million cell updates/sec

Title: us-09-784-340-2
Perfect score: 2802
Sequence: 1 MRSDKSALVFLLLQLFCVGC.....KCFLFSCQKFNKTRKIEKRE 527

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1 seqs, 1636 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=soft -Q=us-09-784-340-2 -DB=us-10-258-080-11
-SUFFIX=pto -OUT=align2_080-11 -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO_XLPXY
-NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : us-10-258-080-11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2802	100.0	1636	1	us-10-258-080-11	

ALIGNMENTS

RESULT 1
us-10-258-080-11

Alignment Scores:

Pred. No.:	0	Length:	1636
Score:	2802.00	Matches:	527
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

us-09-784-340-2 (1-527) x us-10-258-080-11 (1-1636)

```
Qy          1 MetArgSerAspLysSerAlaLeuValPheLeuLeuLeuGlnLeuPheCysValGlyCys 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 ATGAGGTCTGACAAGTCAGCTTTGGTATTTCTGCTCCTGCAGCTCTTCTGTGTTGGCTGT 86

Qy         21 GlyPheCysGlyLysValLeuValTrpProCysAspMetSerHisTrpLeuAsnValLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 GGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTGACATGAGCCATTGGCTTAATGTCAAG 146

Qy         41 ValIleLeuGluGluLeuIleValArgGlyHisGluValThrValLeuThrHisSerLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 GTCATTCTAGAAGAGCTCATAGTGAGAGGCCATGAGGTAACAGTATTGACTCACTCAAAG 206

Qy         61 ProSerLeuIleAspTyrArgLysProSerAlaLeuLysPheGluValValHisMetPro 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 CCTTCGTTAATTGACTACAGGAAGCCTTCTGCATTGAAATTTGAGGTGGTCCATATGCCA 266

Qy         81 GlnAspArgThrGluGluAsnGluIlePheValAspLeuAlaLeuAsnValLeuProGly 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 CAGGACAGAACAGAAGAAAATGAAATATTTGTTGACCTAGCTCTGAATGTCTTGCCAGGC 326

Qy        101 LeuSerThrTrpGlnSerValIleLysLeuAsnAspPhePheValGluIleArgGlyThr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TTATCAACCTGGCAATCAGTTATAAAATTAAATGATTTTTTTGTTGAAATAAGAGGAACT 386

Qy        121 LeuLysMetMetCysGluSerPheIleTyrAsnGlnThrLeuMetLysLysLeuGlnGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 TTAAAAATGATGTGTGAGAGCTTTATCTACAATCAGACGCTTATGAAGAAGCTACAGGAA 446

Qy        141 ThrAsnTyrAspValMetLeuIleAspProValIleProCysGlyAspLeuMetAlaGlu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 ACCAACTACGATGTAATGCTTATAGACCCTGTGATTCCCTGTGGAGACCTGATGGCTGAG 506

Qy        161 LeuLeuAlaValProPheValLeuThrLeuArgIleSerValGlyGlyAsnMetGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 TTGCTTGCAGTCCCTTTTGTGCTCACACTTAGAATTTCTGTAGGAGGCAATATGGAGCGA 566

Qy        181 SerCysGlyLysLeuProAlaProLeuSerTyrValProValProMetThrGlyLeuThr 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 AGCTGTGGGAAACTTCCAGCTCCACTTTCCTATGTACCTGTGCCTATGACAGGACTAACA 626

Qy        201 AspArgMetThrPheLeuGluArgValLysAsnSerMetLeuSerValLeuPheHisPhe 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 GACAGAATGACCTTTCTGGAAAGAGTAAAAAATTCAATGCTTTCAGTTTTGTTCCACTTC 686

Qy        221 TrpIleGlnAspTyrAspTyrHisPheTrpGluGluPheTyrSerLysAlaLeuGlyArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TGGATTCAGGATTACGACTATCATTTTTGGGAAGAGTTTTATAGTAAGGCATTAGGAAGG 746

Qy        241 ProThrThrLeuCysGluThrValGlyLysAlaGluIleTrpLeuIleArgThrTyrTrp 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 CCCACTACATTATGTGAGACTGTGGGAAAAGCTGAGATATGGCTAATACGAACATATTGG 806

Qy        261 AspPheGluPheProGlnProTyrGlnProAsnPheGluPheValGlyGlyLeuHisCys 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 GATTTTGAATTTCCTCAACCATACCAACCTAACTTTGAGTTTGTTGGAGGATTGCACTGT 866

Qy        281 LysProAlaLysAlaLeuProLysGluMetGluAsnPheValGlnSerSerGlyGluAsp 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 AAACCTGCCAAAGCTTTGCCTAAGGAAATGGAAAATTTTGTCCAGAGTTCAGGGGAAGAT 926

Qy        301 GlyIleValValPheSerLeuGlySerLeuPheGlnAsnValThrGluGluLysAlaAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 GGTATTGTGGTGTTTTCTCTGGGGTCACTGTTTCAAAATGTTACAGAAGAAAAGGCTAAT 986

Qy        321 IleIleAlaSerAlaLeuAlaGlnIleProGlnLysValLeuTrpArgTyrLysGlyLys 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATCATTGCTTCAGCCCTTGCCCAGATCCCACAGAAGGTGTTATGGAGGTACAAAGGAAAA 1046

Qy        341 LysProSerThrLeuGlyAlaAsnThrArgLeuTyrAspTrpIleProGlnAsnAspLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1047 AAACCATCCACATTAGGAGCCAATACTCGGCTGTATGATTGGATACCCCAGAATGATCTT 1106

Qy        361 LeuGlyHisProLysThrLysAlaPheIleThrHisGlyGlyMetAsnGlyIleTyrGlu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1107 CTTGGTCATCCCAAAACCAAAGCTTTTATCACTCATGGTGGAATGAATGGGATCTATGAA 1166
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Qy        381 AlaIleTyrHisGlyValProMetValGlyValProIlePheGlyAspGlnLeuAspAsn 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1167 GCTATTTACCATGGGGTCCCTATGGTGGGAGTTCCCATATTTGGTGATCAGCTTGATAAC 1226

Qy        401 IleAlaHisMetLysAlaLysGlyAlaAlaValGluIleAsnPheLysThrMetThrSer 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1227 ATAGCTCACATGAAGGCCAAAGGAGCAGCTGTAGAAATAAACTTCAAAACTATGACAAGC 1286

Qy        421 GluAspLeuLeuArgAlaLeuArgThrValIleThrAspSerSerTyrLysGluAsnAla 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1287 GAAGATTTACTGAGGGCTTTGAGAACAGTCATTACCGATTCCTCTTATAAAGAGAATGCT 1346

Qy        441 MetArgLeuSerArgIleHisHisAspGlnProValLysProLeuAspArgAlaValPhe 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1347 ATGAGATTATCAAGAATTCACCATGATCAACCTGTAAAGCCCCTAGATCGAGCAGTCTTC 1406

Qy        461 TrpIleGluPheValMetArgHisLysGlyAlaLysHisLeuArgSerAlaAlaHisAsp 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1407 TGGATCGAGTTTGTCATGCGCCACAAAGGAGCCAAGCACCTGCGATCAGCTGCCCATGAC 1466

Qy        481 LeuThrTrpPheGlnHisTyrSerIleAspValIleGlyPheLeuLeuThrCysValAla 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1467 CTCACCTGGTTCCAGCACTACTCTATAGATGTGATTGGGTTCCTGCTGACCTGTGTGGCA 1526

Qy        501 ThrAlaIlePheLeuPheThrLysCysPheLeuPheSerCysGlnLysPheAsnLysThr 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1527 ACTGCTATATTCTTGTTCACAAAATGTTTTTTATTTTCCTGTCAAAAATTTAATAAAACT 1586

Qy        521 ArgLysIleGluLysArgGlu 527
              |||||||||||||||||||||
Db       1587 AGAAAGATAGAAAAGAGGGAA 1607
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Search completed: April 29, 2004, 08:35:49
Job time : 2 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2004, 08:33:36 ; Search time 1 Seconds
(without alignments)
3.135 Million cell updates/sec

Title: us-09-784-340-2
Perfect score: 2802
Sequence: 1 MRSDKSALVFLLLQLFCVGC.....KCFLFSCQKFNKTRKIEKRE 527

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1 seqs, 2974 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=soft -Q=us-09-784-340-2 -DB=us-10-206-915-521
-SUFFIX=pto -OUT=align2_915-521 -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO_XLPXY
-NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : us-10-206-915-521:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2802	100.0	2974	1	us-10-206-915-521	

ALIGNMENTS

RESULT 1
us-10-206-915-521

Alignment Scores:

Pred. No.:	0	Length:	2974
Score:	2802.00	Matches:	527
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

us-09-784-340-2 (1-527) x us-10-206-915-521 (1-2974)

```
Qy          1 MetArgSerAspLysSerAlaLeuValPheLeuLeuLeuGlnLeuPheCysValGlyCys 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 ATGAGGTCTGACAAGTCAGCTTTGGTATTTCTGCTCCTGCAGCTCTTCTGTGTTGGCTGT 86

Qy         21 GlyPheCysGlyLysValLeuValTrpProCysAspMetSerHisTrpLeuAsnValLys 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 GGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTGACATGAGCCATTGGCTTAATGTCAAG 146

Qy         41 ValIleLeuGluGluLeuIleValArgGlyHisGluValThrValLeuThrHisSerLys 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 GTCATTCTAGAAGAGCTCATAGTGAGAGGCCATGAGGTAACAGTATTGACTCACTCAAAG 206

Qy         61 ProSerLeuIleAspTyrArgLysProSerAlaLeuLysPheGluValValHisMetPro 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 CCTTCGTTAATTGACTACAGGAAGCCTTCTGCATTGAAATTTGAGGTGGTCCATATGCCA 266

Qy         81 GlnAspArgThrGluGluAsnGluIlePheValAspLeuAlaLeuAsnValLeuProGly 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 CAGGACAGAACAGAAGAAAATGAAATATTTGTTGACCTAGCTCTGAATGTCTTGCCAGGC 326

Qy        101 LeuSerThrTrpGlnSerValIleLysLeuAsnAspPheValGluIleArgGlyThr 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TTATCAACCTGGCAATCAGTTATAAAATTAAATGATTTTTTGTTGAAATAAGAGGAACT 386

Qy        121 LeuLysMetMetCysGluSerPheIleTyrAsnGlnThrLeuMetLysLysLeuGlnGlu 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 TTAAAAATGATGTGTGAGAGCTTTATCTACAATCAGACGCTTATGAAGAAGCTACAGGAA 446

Qy        141 ThrAsnTyrAspValMetLeuIleAspProValIleProCysGlyAspLeuMetAlaGlu 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 ACCAACTACGATGTAATGCTTATAGACCCTGTGATTCCCTGTGGAGACCTGATGGCTGAG 506

Qy        161 LeuLeuAlaValProPheValLeuThrLeuArgIleSerValGlyGlyAsnMetGluArg 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 TTGCTTGCAGTCCCTTTTGTGCTCACACTTAGAATTTCTGTAGGAGGCAATATGGAGCGA 566

Qy        181 SerCysGlyLysLeuProAlaProLeuSerTyrValProValProMetThrGlyLeuThr 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 AGCTGTGGGAAACTTCCAGCTCCACTTTCCTATGTACCTGTGCCTATGACAGGACTAACA 626

Qy        201 AspArgMetThrPheLeuGluArgValLysAsnSerMetLeuSerValLeuPheHisPhe 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 GACAGAATGACCTTTCTGGAAAGAGTAAAAAATTCAATGCTTTCAGTTTTGTTCCACTTC 686

Qy        221 TrpIleGlnAspTyrAspTyrHisPheTrpGluGluPheTyrSerLysAlaLeuGlyArg 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TGGATTCAGGATTACGACTATCATTTTTGGGAAGAGTTTTATAGTAAGGCATTAGGAAGG 746

Qy        241 ProThrThrLeuCysGluThrValGlyLysAlaGluIleTrpLeuIleArgThrTyrTrp 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 CCCACTACATTATGTGAGACTGTGGGAAAAGCTGAGATATGGCTAATACGAACATATTGG 806

Qy        261 AspPheGluPheProGlnProTyrGlnProAsnPheGluPheValGlyGlyLeuHisCys 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 GATTTTGAATTTCCTCAACCATACCAACCTAACTTTGAGTTTGTTGGAGGATTGCACTGT 866

Qy        281 LysProAlaLysAlaLeuProLysGluMetGluAsnPheValGlnSerSerGlyGluAsp 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 AAACCTGCCAAAGCTTTGCCTAAGGAAATGGAAAATTTTGTCCAGAGTTCAGGGGAAGAT 926

Qy        301 GlyIleValValPheSerLeuGlySerLeuPheGlnAsnValThrGluGluLysAlaAsn 320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 GGTATTGTGGTGTTTTCTCTGGGGTCACTGTTTCAAAATGTTACAGAAGAAAAGGCTAAT 986

Qy        321 IleIleAlaSerAlaLeuAlaGlnIleProGlnLysValLeuTrpArgTyrLysGlyLys 340
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATCATTGCTTCAGCCCTTGCCCAGATCCCACAGAAGGTGTTATGGAGGTACAAAGGAAAA 1046

Qy        341 LysProSerThrLeuGlyAlaAsnThrArgLeuTyrAspTrpIleProGlnAsnAspLeu 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1047 AAACCATCCACATTAGGAGCCAATACTCGGCTGTATGATTGGATACCCCAGAATGATCTT 1106

Qy        361 LeuGlyHisProLysThrLysAlaPheIleThrHisGlyGlyMetAsnGlyIleTyrGlu 380
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1107 CTTGGTCATCCCAAAACCAAAGCTTTTATCACTCATGGTGGAATGAATGGGATCTATGAA 1166
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```
Qy        381 AlaIleTyrHisGlyValProMetValGlyValProIlePheGlyAspGlnLeuAspAsn 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1167 GCTATTTACCATGGGGTCCCTATGGTGGGAGTTCCCATATTTGGTGATCAGCTTGATAAC 1226

Qy        401 IleAlaHisMetLysAlaLysGlyAlaAlaValGluIleAsnPheLysThrMetThrSer 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1227 ATAGCTCACATGAAGGCCAAAGGAGCAGCTGTAGAAATAAACTTCAAAACTATGACAAGC 1286

Qy        421 GluAspLeuLeuArgAlaLeuArgThrValIleThrAspSerSerTyrLysGluAsnAla 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1287 GAAGATTTACTGAGGGCTTTGAGAACAGTCATTACCGATTCCTCTTATAAAGAGAATGCT 1346

Qy        441 MetArgLeuSerArgIleHisHisAspGlnProValLysProLeuAspArgAlaValPhe 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1347 ATGAGATTATCAAGAATTCACCATGATCAACCTGTAAAGCCCCTAGATCGAGCAGTCTTC 1406

Qy        461 TrpIleGluPheValMetArgHisLysGlyAlaLysHisLeuArgSerAlaAlaHisAsp 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1407 TGGATCGAGTTTGTCATGCGCCACAAAGGAGCCAAGCACCTGCGATCAGCTGCCCATGAC 1466

Qy        481 LeuThrTrpPheGlnHisTyrSerIleAspValIleGlyPheLeuLeuThrCysValAla 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1467 CTCACCTGGTTCCAGCACTACTCTATAGATGTGATTGGGTTCCTGCTGACCTGTGTGGCA 1526

Qy        501 ThrAlaIlePheLeuPheThrLysCysPheLeuPheSerCysGlnLysPheAsnLysThr 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1527 ACTGCTATATTCTTGTTCACAAAATGTTTTTTATTTTCCTGTCAAAAATTTAATAAAACT 1586

Qy        521 ArgLysIleGluLysArgGlu 527
              |||||||||||||||||||||
Db       1587 AGAAAGATAGAAAAGAGGGAA 1607
```

Search completed: April 29, 2004, 08:33:39
Job time : 3 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2004, 08:27:53 ; Search time 4 Seconds
(without alignments)
4.103 Million cell updates/sec

Title: us-09-784-340-1
Perfect score: 2759
Sequence: 1 caaccattgcagatcagtgt.....ctgtcagccgttacgtagcg 2759

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 2974 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : us-10-206-915-521:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2335	84.6	2974	1	us-10-206-915-521	

ALIGNMENTS

RESULT 1
us-10-206-915-521

Query Match 84.6%; Score 2335; DB 1; Length 2974;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 2441; Conservative 0; Mismatches 85; Indels 10; Gaps 5;

```
Qy    12 GATCAGTGTGTGAGGGAACTGCCATCATGAGGTCTGACAAGTCAGCTTTGGTATTTCTGC 71
Db     1 GATCAGTGTGTGAGGGAACTGCCATCATGAGGTCTGACAAGTCAGCTTTGGTATTTCTGC 60

Qy    72 TCCTGCAGCTCTTCTGTGTTGGCTGTGGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTG 131
Db    61 TCCTGCAGCTCTTCTGTGTTGGCTGTGGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTG 120

Qy   132 ACATGAGCCATTGGCTTAATGTCAAGGTCATTCTAGAAGAGCTCATAGTGAGAGGCCATG 191
Db   121 ACATGAGCCATTGGCTTAATGTCAAGGTCATTCTAGAAGAGCTCATAGTGAGAGGCCATG 180

Qy   192 AGGTAACAGTATTGACTCACTCAAAGCCTTCGTTAATTGACTACAGGAAGCCTTCTGCAT 251
Db   181 AGGTAACAGTATTGACTCACTCAAAGCCTTCGTTAATTGACTACAGGAAGCCTTCTGCAT 240

Qy   252 TGAAATTTGAGGTGGTCCATATGCCACAGGACAGAACAGAAGAAAATGAAATATTTGTTG 311
Db   241 TGAAATTTGAGGTGGTCCATATGCCACAGGACAGAACAGAAGAAAATGAAATATTTGTTG 300

Qy   312 ACCTAGCTCTGAATGTCTTGCCAGGCTTATCAACCTGGCAATCAGTTATAAAATTAAATG 371
Db   301 ACCTAGCTCTGAATGTCTTGCCAGGCTTATCAACCTGGCAATCAGTTATAAAATTAAATG 360

Qy   372 ATTTTTTTGTTGAAATAAGAGGAACTTTAAAAATGATGTGTGAGAGCTTTATCTACAATC 431
Db   361 ATTTTTTTGTTGAAATAAGAGGAACTTTAAAAATGATGTGTGAGAGCTTTATCTACAATC 420

Qy   432 AGACGCTTATGAAGAAGCTACAGGAAACCAACTACGATGTAATGCTTATAGACCCTGTGA 491
Db   421 AGACGCTTATGAAGAAGCTACAGGAAACCAACTACGATGTAATGCTTATAGACCCTGTGA 480

Qy   492 TTCCCTGTGGAGACCTGATGGCTGAGTTGCTTGCAGTCCCTTTTGTGCTCACACTTAGAA 551
Db   481 TTCCCTGTGGAGACCTGATGGCTGAGTTGCTTGCAGTCCCTTTTGTGCTCACACTTAGAA 540

Qy   552 TTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAAACTTCCAGCTCCACTTTCCTATG 611
Db   541 TTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAAACTTCCAGCTCCACTTTCCTATG 600

Qy   612 TACCTGTGCCTATGACAGGACTAACAGACAGAATGACCTTTCTGGAAAGAGTAAAAAATT 671
Db   601 TACCTGTGCCTATGACAGGACTAACAGACAGAATGACCTTTCTGGAAAGAGTAAAAAATT 660

Qy   672 CAATGCTTTCAGTTTTGTTCCACTTCTGGATTCAGGATTACGACTATCATTTTTGGGAAG 731
Db   661 CAATGCTTTCAGTTTTGTTCCACTTCTGGATTCAGGATTACGACTATCATTTTTGGGAAG 720

Qy   732 AGTTTTATAGTAAGGCATTAGGAAGGCCCACTACATTATGTGAGACTGTGGGAAAAGCTG 791
Db   721 AGTTTTATAGTAAGGCATTAGGAAGGCCCACTACATTATGTGAGACTGTGGGAAAAGCTG 780

Qy   792 AGATATGGCTAATACGAACATATTGGGATTTTGAATTTCCTCAACCATACCAACCTAACT 851
Db   781 AGATATGGCTAATACGAACATATTGGGATTTTGAATTTCCTCAACCATACCAACCTAACT 840

Qy   852 TTGAGTTTGTTGGAGGATTGCACTGTAAACCTGCCAAAGCTTTGCCTAAGGAAATGGAAA 911
Db   841 TTGAGTTTGTTGGAGGATTGCACTGTAAACCTGCCAAAGCTTTGCCTAAGGAAATGGAAA 900

Qy   912 ATTTTGTCCAGAGTTCAGGGGAAGATGGTATTGTGGTGTTTTCTCTGGGGTCACTGTTTC 971
Db   901 ATTTTGTCCAGAGTTCAGGGGAAGATGGTATTGTGGTGTTTTCTCTGGGGTCACTGTTTC 960

Qy   972 AAAATGTTACAGAAGAAAAGGCTAATATCATTGCTTCAGCCCTTGCCCAGATCCCACAGA 1031
Db   961 AAAATGTTACAGAAGAAAAGGCTAATATCATTGCTTCAGCCCTTGCCCAGATCCCACAGA 1020

Qy  1032 AGGTGTTATGGAGGTACAAAGGAAAAAAACCATCCACATTAGGAGCCAATACTCGGCTGT 1091
Db  1021 AGGTGTTATGGAGGTACAAAGGAAAAAAACCATCCACATTAGGAGCCAATACTCGGCTGT 1080

Qy  1092 ATGATTGGATACCCCAGAATGATCTTCTTGGTCATCCCAAAACCAAAGCTTTTATCACTC 1151
Db  1081 ATGATTGGATACCCCAGAATGATCTTCTTGGTCATCCCAAAACCAAAGCTTTTATCACTC 1140

Qy  1152 ATGGTGGAATGAATGGGATCTATGAAGCTATTTACCATGGGGTCCCTATGGTGGGAGTTC 1211
Db  1141 ATGGTGGAATGAATGGGATCTATGAAGCTATTTACCATGGGGTCCCTATGGTGGGAGTTC 1200

Qy  1212 CCATATTTGGTGATCAGCTTGATAACATAGCTCACATGAAGGCCAAAGGAGCAGCTGTAG 1271
Db  1201 CCATATTTGGTGATCAGCTTGATAACATAGCTCACATGAAGGCCAAAGGAGCAGCTGTAG 1260

Qy  1272 AAATAAACTTCAAAACTATGACAAGCGAAGATTTACTGAGGGCTTTGAGAACAGTCATTA 1331
Db  1261 AAATAAACTTCAAAACTATGACAAGCGAAGATTTACTGAGGGCTTTGAGAACAGTCATTA 1320

Qy  1332 CCGATTCCTCTTATAAAGAGAATGCTATGAGATTATCAAGAATTCACCATGATCAACCTG 1391
Db  1321 CCGATTCCTCTTATAAAGAGAATGCTATGAGATTATCAAGAATTCACCATGATCAACCTG 1380

Qy  1392 TAAAGCCCCTAGATCGAGCAGTCTTCTGGATCGAGTTTGTCATGCGCCACAAAGGAGCCA 1451
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Db       1381 TAAAGCCCCTAGATCGAGCAGTCTTCTGGATCGAGTTTGTCATGCGCCACAAAGGAGCCA 1440
Qy       1452 AGCACCTGCGATCAGCTGCCCATGACCTCACCTGGTTCCAGCACTACTCTATAGATGTGA 1511
Db       1441 AGCACCTGCGATCAGCTGCCCATGACCTCACCTGGTTCCAGCACTACTCTATAGATGTGA 1500
Qy       1512 TTGGGTTCCTGCTGACCTGTGTGGCAACTGCTATATTCTTGTTCACAAAATGTTTTTTAT 1571
Db       1501 TTGGGTTCCTGCTGACCTGTGTGGCAACTGCTATATTCTTGTTCACAAAATGTTTTTTAT 1560
Qy       1572 TTTCCTGTCAAAAATTTAATAAAACTAGAAAGATAGAAAAGAGGGAATAGATCTTTCCAA 1631
Db       1561 TTTCCTGTCAAAAATTTAATAAAACTAGAAAGATAGAAAAGAGGGAATAGATCTTTCCAA 1620
Qy       1632 ATTCAAGAAAGACCTGATGGGGTAATCCTGTTAATTCCAGCCACATAGAATTTGGTGAAA 1691
Db       1621 ATTCAAGAAAGACCTGATGGGGTAATCCTGTTAATTCCAGCCACATAGAATTTGGTGAAA 1680
Qy       1692 ACCTTGCTATTTTCATATTATCTATTCTGTTATTTTATCTTAGCTATATAGCCTAGAATT 1751
Db       1681 ACCTTGCTATTTTCATATTATCTATTCTGTTATTTTATCTTAGCTATATAGCCTAGAATT 1740
Qy       1752 CCATGATCATGAGGTTGTGAGTATATCTCATTCTTTCGTTGCATTTTCCTAGGTGTGCTT 1811
Db       1741 CCATGATCATGAGGTTGTGAGTATATCTCATTCTTTCGTTGTATTTTCCTAGGTGTCTTT 1800
Qy       1812 ACTCTCTTCTCTCACTTTGTGACACAAGGACATGAATACATCTAAATTTTCCTATTTCTG 1871
Db       1801 ACTCTCTTCTCTCACTTTGTGACACAAGGACATGAATACATCTAAATTTTCCTATTTCTG 1860
Qy       1872 ATATCACTGTTTCCATGACGTCATTACTTCTCTAACCTTAAGTGATAGGGTGACCTGCAA 1931
Db       1861 ATATGACTGTTTTGATGATGTCATTACTTCTATAACCTTAAGTGATAGGGTGACATGCAA 1920
Qy       1932 TATGCTGATTCCTGGTGTTTGCACAAACACATGGATGTAAAGAAGTAAAAAATGTAAAAT 1991
Db       1921 TATGATTATTCCTGGTGTGCGCCCAAACACATGGATATAAAGAGGTAAAAAACTTAAAAT 1980
Qy       1992 TCACAAAATTCAGTAAACCACACAAATCAATGAAGCATTCTATGACATTAGCTTGTTATG 2051
Db       1981 TCACAAAATTCAGTAAACCACACAAATCAGGTAAGTGTTCTATGAGATTAGCTGGCTATG 2040
Qy       2052 AGTAACATAATGATTTTTCTTTTTCAATTTAAATAAGCCCTTCTACATACCCAGCATTAC 2111
Db       2041 AGAAACATAATGATGTTTCTTTTTCAATTTAAATAAGCCTTTCTACATAGCCAGCATCAG 2100
Qy       2112 TGATCTCAGACAATGAATTGCTAAAAATGACGATAGGGCATTACACTCAGAATAGTTTGC 2171
Db       2101 TGATCTCAGAAAATAAATTGCTAATAATGATGACATGGCATTATGCTTAGAAAAGTTTGC 2160
Qy       2172 TATATTTCCACATACCTCATCTAGATGTCATAGCCTACATTTCTGCCATCACTTAACTGA 2231
Db       2161 TGTATTTCCATAGACCTCATCTAGATGTCATGGCCTACATTTCTGCCATCACTCAACCAA 2220
Qy       2232 CA-TTTTTTGTGTGTTCTTGATGATAAATAGACAGTTCTTATTATTGTCCTCAAATAATA 2290
Db       2221 TACTTTTTTCTGTTTTCTTGATGATAAAAAGACCTTTCTCATGATTGCCATCAAATAACA 2280
Qy       2291 AAAGAAACT-GAAATTTTCTTACATAGAGAAAATGTCCATAAGATATTCAAGTTAAACAG 2349
Db       2281 AAAGAAACTATTTTTTTTCTCACATAGAGAACATGTCAGTAAGATATTCAAGGTGAACAG 2340
Qy       2350 ATTATTTTGAGATAAGTAACCATTAGAAATATGTGATTGTAATTTCTGATTTTATAAAAT 2409
Db       2341 ATATTTTTGGGATTAGTAACTATTTGAAATATGTGGTGATAATTACTGAGTTTATAAAA- 2399
Qy       2410 TTTAATTGATAGTACACTT------GATTTAAATGTCTATTCTTT-AAAATGATGAATAC 2462
Db       2400 TTTATTTGATAGTACACTTAAAGAAGATTTATATGTTTATTCTTTAAAAATGATGAATAC 2459
Qy       2463 TCATAATTCTTATCTCTATAATCAAAAGTATAATTTACTGTAGAAAAATAAAGAGATGCT 2522
Db       2460 TCATAATTCTTATCTCTATAATCAAAAGTATAATTTACTGTAGAAAAATAAAGAGATGCT 2519
Qy       2523 TGTTCTGAAAGTAAAA 2538
Db       2520 TGTTCTGAAAGTAAGA 2535
```

Search completed: April 29, 2004, 08:27:58
Job time : 5 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2004, 08:30:18 ; Search time 2 Seconds
(without alignments)
4.514 Million cell updates/sec

Title: us-09-784-340-1
Perfect score: 2759
Sequence: 1 caaccattgcagatcagtgt.....ctgtcagccgttacgtagcg 2759

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1636 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : us-10-258-080-11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1636	59.3	1636	1	us-10-258-080-11	

ALIGNMENTS

RESULT 1
us-10-258-080-11

Query Match 59.3%; Score 1636; DB 1; Length 1636;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          12 GATCAGTGTGTGAGGGAACTGCCATCATGAGGTCTGACAAGTCAGCTTTGGTATTTCTGC  71
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GATCAGTGTGTGAGGGAACTGCCATCATGAGGTCTGACAAGTCAGCTTTGGTATTTCTGC  60

Qy          72 TCCTGCAGCTCTTCTGTGTTGGCTGTGGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTG 131
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TCCTGCAGCTCTTCTGTGTTGGCTGTGGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTG 120

Qy         132 ACATGAGCCATTGGCTTAATGTCAAGGTCATTCTAGAAGAGCTCATAGTGAGAGGCCATG 191
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 ACATGAGCCATTGGCTTAATGTCAAGGTCATTCTAGAAGAGCTCATAGTGAGAGGCCATG 180

Qy         192 AGGTAACAGTATTGACTCACTCAAAGCCTTCGTTAATTGACTACAGGAAGCCTTCTGCAT 251
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 AGGTAACAGTATTGACTCACTCAAAGCCTTCGTTAATTGACTACAGGAAGCCTTCTGCAT 240

Qy         252 TGAAATTTGAGGTGGTCCATATGCCACAGGACAGAACAGAAGAAAATGAAATATTTGTTG 311
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TGAAATTTGAGGTGGTCCATATGCCACAGGACAGAACAGAAGAAAATGAAATATTTGTTG 300

Qy         312 ACCTAGCTCTGAATGTCTTGCCAGGCTTATCAACCTGGCAATCAGTTATAAAATTAAATG 371
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ACCTAGCTCTGAATGTCTTGCCAGGCTTATCAACCTGGCAATCAGTTATAAAATTAAATG 360

Qy         372 ATTTTTTTGTTGAAATAAGAGGAACTTTAAAAATGATGTGTGAGAGCTTTATCTACAATC 431
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 ATTTTTTTGTTGAAATAAGAGGAACTTTAAAAATGATGTGTGAGAGCTTTATCTACAATC 420

Qy         432 AGACGCTTATGAAGAAGCTACAGGAAACCAACTACGATGTAATGCTTATAGACCCTGTGA 491
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 AGACGCTTATGAAGAAGCTACAGGAAACCAACTACGATGTAATGCTTATAGACCCTGTGA 480

Qy         492 TTCCCTGTGGAGACCTGATGGCTGAGTTGCTTGCAGTCCCTTTTGTGCTCACACTTAGAA 551
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 TTCCCTGTGGAGACCTGATGGCTGAGTTGCTTGCAGTCCCTTTTGTGCTCACACTTAGAA 540

Qy         552 TTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAAACTTCCAGCTCCACTTTCCTATG 611
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAAACTTCCAGCTCCACTTTCCTATG 600

Qy         612 TACCTGTGCCTATGACAGGACTAACAGACAGAATGACCTTTCTGGAAAGAGTAAAAAATT 671
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 TACCTGTGCCTATGACAGGACTAACAGACAGAATGACCTTTCTGGAAAGAGTAAAAAATT 660

Qy         672 CAATGCTTTCAGTTTTGTTCCACTTCTGGATTCAGGATTACGACTATCATTTTTGGGAAG 731
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAATGCTTTCAGTTTTGTTCCACTTCTGGATTCAGGATTACGACTATCATTTTTGGGAAG 720

Qy         732 AGTTTTATAGTAAGGCATTAGGAAGGCCCACTACATTATGTGAGACTGTGGGAAAAGCTG 791
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 AGTTTTATAGTAAGGCATTAGGAAGGCCCACTACATTATGTGAGACTGTGGGAAAAGCTG 780

Qy         792 AGATATGGCTAATACGAACATATTGGGATTTTGAATTTCCTCAACCATACCAACCTAACT 851
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AGATATGGCTAATACGAACATATTGGGATTTTGAATTTCCTCAACCATACCAACCTAACT 840

Qy         852 TTGAGTTTGTTGGAGGATTGCACTGTAAACCTGCCAAAGCTTTGCCTAAGGAAATGGAAA 911
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 TTGAGTTTGTTGGAGGATTGCACTGTAAACCTGCCAAAGCTTTGCCTAAGGAAATGGAAA 900

Qy         912 ATTTTGTCCAGAGTTCAGGGGAAGATGGTATTGTGGTGTTTTCTCTGGGGTCACTGTTTC 971
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 ATTTTGTCCAGAGTTCAGGGGAAGATGGTATTGTGGTGTTTTCTCTGGGGTCACTGTTTC 960

Qy         972 AAAATGTTACAGAAGAAAAGGCTAATATCATTGCTTCAGCCCTTGCCCAGATCCCACAGA 1031
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 AAAATGTTACAGAAGAAAAGGCTAATATCATTGCTTCAGCCCTTGCCCAGATCCCACAGA 1020

Qy        1032 AGGTGTTATGGAGGTACAAAGGAAAAAAAACCATCCACATTAGGAGCCAATACTCGGCTGT 1091
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 AGGTGTTATGGAGGTACAAAGGAAAAAAAACCATCCACATTAGGAGCCAATACTCGGCTGT 1080

Qy        1092 ATGATTGGATACCCCAGAATGATCTTCTTGGTCATCCCAAAACCAAAGCTTTTATCACTC 1151
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 ATGATTGGATACCCCAGAATGATCTTCTTGGTCATCCCAAAACCAAAGCTTTTATCACTC 1140

Qy        1152 ATGGTGGAATGAATGGGATCTATGAAGCTATTTACCATGGGGTCCCTATGGTGGGAGTTC 1211
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 ATGGTGGAATGAATGGGATCTATGAAGCTATTTACCATGGGGTCCCTATGGTGGGAGTTC 1200

Qy        1212 CCATATTTGGTGATCAGCTTGATAACATAGCTCACATGAAGGCCAAAGGAGCAGCTGTAG 1271
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 CCATATTTGGTGATCAGCTTGATAACATAGCTCACATGAAGGCCAAAGGAGCAGCTGTAG 1260

Qy        1272 AAATAAACTTCAAAACTATGACAAGCGAAGATTTACTGAGGGCTTTGAGAACAGTCATTA 1331
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 AAATAAACTTCAAAACTATGACAAGCGAAGATTTACTGAGGGCTTTGAGAACAGTCATTA 1320

Qy        1332 CCGATTCCTCTTATAAAGAGAATGCTATGAGATTATCAAGAATTCACCATGATCAACCTG 1391
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 CCGATTCCTCTTATAAAGAGAATGCTATGAGATTATCAAGAATTCACCATGATCAACCTG 1380

Qy        1392 TAAAGCCCCTAGATCGAGCAGTCTTCTGGATCGAGTTTGTCATGCGCCACAAAGGAGCCA 1451
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TAAAGCCCCTAGATCGAGCAGTCTTCTGGATCGAGTTTGTCATGCGCCACAAAGGAGCCA 1440

Qy       1452 AGCACCTGCGATCAGCTGCCCATGACCTCACCTGGTTCCAGCACTACTCTATAGATGTGA 1511
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AGCACCTGCGATCAGCTGCCCATGACCTCACCTGGTTCCAGCACTACTCTATAGATGTGA 1500

Qy       1512 TTGGGTTCCTGCTGACCTGTGTGGCAACTGCTATATTCTTGTTCACAAAATGTTTTTTAT 1571
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TTGGGTTCCTGCTGACCTGTGTGGCAACTGCTATATTCTTGTTCACAAAATGTTTTTTAT 1560

Qy       1572 TTTCCTGTCAAAAATTTAATAAAACTAGAAAGATAGAAAAGAGGGAATAGATCTTTCCAA 1631
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TTTCCTGTCAAAAATTTAATAAAACTAGAAAGATAGAAAAGAGGGAATAGATCTTTCCAA 1620

Qy       1632 ATTCAAGAAAGACCTG 1647
                ||||||||||||||||
Db       1621 ATTCAAGAAAGACCTG 1636
```

Search completed: April 29, 2004, 08:30:21
Job time : 3 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 29, 2004, 08:22:55 ; Search time 0.001 Seconds
(without alignments)
277.729 Million cell updates/sec

Title: us-09-784-340-2
Perfect score: 2802
Sequence: 1 MRSDKSALVFLLLQLFCVGC.....KCFLFSCQKFNKTRKIEKRE 527

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 527 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : us-10-206-915-522:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2802	100.0	527	1	us-10-206-915-522	

ALIGNMENTS

RESULT 1
us-10-206-915-522

Query Match 100.0%; Score 2802; DB 1; Length 527;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRSDKSALVFLLLQLFCVGCGPCGKVLVWPCDMSHWLNVKVILEELIVRGHEVTVLTHSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRSDKSALVFLLLQLFCVGCGPCGKVLVWPCDMSHWLNVKVILEELIVRGHEVTVLTHSK 60

Qy         61 PSLIDYRKPSALKFEVVHMPQDRTEENEIFVDLALNVLPGLSTWQSVIKLNDFFVEIRGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PSLIDYRKPSALKFEVVHMPQDRTEENEIFVDLALNVLPGLSTWQSVIKLNDFFVEIRGT 120

Qy        121 LKMMCESFIYNQTLMKKLQETNYDVMLIDPVIPCGDLMAELLAVPFVLTLRISVGGNMER 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LKMMCESFIYNQTLMKKLQETNYDVMLIDPVIPCGDLMAELLAVPFVLTLRISVGGNMER 180

Qy        181 SCGKLPAPLSYVPVPMTGLTDRMTFLERVKNSMLSVLFHFWIQDYDYHFWEEFYSKALGR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SCGKLPAPLSYVPVPMTGLTDRMTFLERVKNSMLSVLFHFWIQDYDYHFWEEFYSKALGR 240

Qy        241 PTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGED 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGED 300

Qy        301 GIVVFSLGSLFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRLYDWIPQNDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GIVVFSLGSLFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRLYDWIPQNDL 360

Qy        361 LGHPKTKAFITHGGMNGIYEAIYHGVPMVGVPIFGDQLDNIAHMKAKGAAVEINFKTMTS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LGHPKTKAFITHGGMNGIYEAIYHGVPMVGVPIFGDQLDNIAHMKAKGAAVEINFKTMTS 420

Qy        421 EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSAAHD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSAAHD 480

Qy        481 LTWFQHYSIDVIGFLLTCVATAIFLFTKCFLFSCQKFNKTRKIEKRE 527
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LTWFQHYSIDVIGFLLTCVATAIFLFTKCFLFSCQKFNKTRKIEKRE 527
```

Search completed: April 29, 2004, 08:22:56
Job time : 1 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 29, 2004, 08:25:24 ; Search time 0.001 Seconds
(without alignments)
277.729 Million cell updates/sec

Title: us-09-784-340-2
Perfect score: 2802
Sequence: 1 MRSDKSALVFLLLQLFCVGC.....KCFLFSCQKFNKTRKIEKRE 527

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 527 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : us-10-258-080-1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2802	100.0	527	1	us-10-258-080-1	

ALIGNMENTS

RESULT 1
us-10-258-080-1

Query Match 100.0%; Score 2802; DB 1; Length 527;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRSDKSALVFLLLQLFCVGCGFCGKVLVWPCDMSHWLNVKVILEELIVRGHEVTVLTHSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRSDKSALVFLLLQLFCVGCGFCGKVLVWPCDMSHWLNVKVILEELIVRGHEVTVLTHSK 60

Qy         61 PSLIDYRKPSALKFEVVHMPQDRTEENEIFVDLALNVLPGLSTWQSVIKLNDFFVEIRGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PSLIDYRKPSALKFEVVHMPQDRTEENEIFVDLALNVLPGLSTWQSVIKLNDFFVEIRGT 120

Qy        121 LKMMCESFIYNQTLMKKLQETNYDVMLIDPVIPCGDLMAELLAVPFVLTLRISVGGNMER 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LKMMCESFIYNQTLMKKLQETNYDVMLIDPVIPCGDLMAELLAVPFVLTLRISVGGNMER 180

Qy        181 SCGKLPAPLSYVPVPMTGLTDRMTFLERVKNSMLSVLFHFWIQDYDYHFWEEFYSKALGR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SCGKLPAPLSYVPVPMTGLTDRMTFLERVKNSMLSVLFHFWIQDYDYHFWEEFYSKALGR 240

Qy        241 PTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGED 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGED 300

Qy        301 GIVVFSLGSLFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRLYDWIPQNDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GIVVFSLGSLFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRLYDWIPQNDL 360

Qy        361 LGHPKTKAFITHGGMNGIYEAIYHGVPMVGVPIFGDQLDNIAHMKAKGAAVEINFKTMTS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LGHPKTKAFITHGGMNGIYEAIYHGVPMVGVPIFGDQLDNIAHMKAKGAAVEINFKTMTS 420

Qy        421 EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSAAHD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSAAHD 480

Qy        481 LTWFQHYSIDVIGFLLTCVATAIFLFTKCFLFSCQKFNKTRKIEKRE 527
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LTWFQHYSIDVIGFLLTCVATAIFLFTKCFLFSCQKFNKTRKIEKRE 527
```

Search completed: April 29, 2004, 08:25:25
Job time : 1 secs

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Db    353 DWIPQNDLLGHPKTKAFITHGGTNGIYEAIYHGVPMVGVPMFADQPDNIAHMKAKGAAVE 412

Qy    413 INFKTMTSEDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAK 472
          :|  |||| |:|| |||||| : |||||||||||||||||||||||||||||||||||||||
Db    413 VNLNTMTSVDLLSALRTVINEPSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAK 472

Qy    473 HLRSAAHDLTWFQHYSIDVIGFLLTCVATAIFLFTKCFLFSCQKFNKTRKIEKRE 527
          ||| |||||||||::|:|||||| || |||||  :| ||||||| |  | :|||
Db    473 HLRVAAHDLTWFQYHSLDVIGFLLVCVTTAIFLVIQCCLFSCQKFGKIGKKKKRE 527


RESULT   4
O75614
ID   O75614      PRELIMINARY;      PRT;   528 AA.
AC   O75614;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   UDP GLUCURONOSYLTRANSFERASE 2B4 PRECURSOR.
GN   UGT2B4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93326164; PubMed=8333863;
RA   Jin C.J., Miners J.O., Lillywhite K.J., Mackenzie P.I.;
RT   "cDNA cloning and expression of two new members of the human liver
RT   UDP-glucuronosyltransferase 2B subfamily.";
RL   Biochem. Biophys. Res. Commun. 194:496-503(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Mackenzie P.I.;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF081793; AAC32272.1; -.
DR   InterPro; IPR002213; -.
DR   Pfam; PF00201; UDPGT; 1.
DR   PROSITE; PS00375; UDPGT; 1.
KW   Transferase.
SQ   SEQUENCE   528 AA;  60497 MW;  B6F5BA0705E952C4 CRC64;


  Query Match             61.1%;  Score 1711;  DB 4;  Length 528;
  Best Local Similarity   62.1%;  Pred. No. 4e-134;
  Matches  328;  Conservative   64;  Mismatches  132;  Indels    4;  Gaps    3;

Qy      3 SDKSALVFLLLQLFC-VGCGFCGKVLVWPCDMSHWLNVKVILEELIVRGHEVTVLTHSKP 61
          | |     ||:|| |    | |||||||| : |||:|:| ||:||: ||||||||  |
Db      2 SMKWTSALLLIQLSCYFSSGSCGKVLVWPTEFSHWMNIKTILDELVQRGHEVTVLASSAS 61

Qy     62 SLIDYRKPSALKFEVVHMPQDRTEENEIFVDLALN--VLPGLSTWQSVIKLNDFFVEIRG 119
             |  || |||||  :   :||  :|  ' |       ||  : |  : :: :
Db     62 ISFDPNSPSTLKFEVYPVSLTKTEFEDIIKQLVKRWAELPKDTFWSYLSQVQEIMWTFND 121

Qy    120 TLKMMCESFIYNQTLMKKLQETNYDVMLIDPVIPCGDLMAELLAVPFVLTLRISVGGNME 179
           |:  |:  : |: |||||||: :||:| | | | |:|:|||| :||| :|| | |  :|
Db    122 ILRKFCKDIVSNKKLMKKLQESRFDVVLADAVFPFGELLAELLKIPFVYSLRFSPGYAIE 181

Qy    180 RSCGKLPAPLSYVPVPMTGLTDRMTFLERVKNSMLSVLFHFWIQDYDYHFWEEFYSKALG 239
          :  | |  | ||||| |: |:|:|||:||||| :  : | || | :|   |::|||: ||
Db    182 KHSGGLLFPPSYVPVVMSELSDQMTFIERVKNMIYVLYFEFWFQIFDMKKWDQFYSEVLG 241

Qy    240 RPTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGE 299
          ||||| ||: ||:|||| ||||:|| |  || |||||||||| |||: : |||||||
Db    242 RPTTLSETMAKADIWLIRNYWDFQFPHPLLPNVEFVGGLHCKPAKPLPKKWKEFVQSSGE 301

Qy    300 DGIVVFSLGSLFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRLYDWIPQND 359
          :|:|||||||:  | :||:||:||||||:||||||||: | || ||| |||| ||||||
Db    302 NGVVVFSLGSMVSNTSEERANVIASALAKIPQKVLWRFDGNKPDTLGLNTRLYKWIPQND 361

Qy    360 LLGHPKTKAFITHGGMNGIYEAIYHGVPMVGVPIFGDQLDNIAHMKAKGAAVEINFKTMT 419
          |||||||:||||||| ||||||||||:||||||:  || |||||||||||| ::| ||:
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```
Db    362 LLGHPKTRAFITHGGANGIYEAIYHGIPMVGVPLLADQPDNIAHMKAKGAAVSLDFHTMS 421

Qy    420 SEDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSAAH 479
          | ||| ||:||| |  |||||||||||||||||||||||||||||||||||||||| |||
Db    422 STDLLNALKTVINDPLYKENAMKLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAAH 481

Qy    480 DLTWFQHYSIDVIGFLLTCVATAIFLFTKCFLFSCQKFNKTRKIEKRE 527
          |||||||::|:|| |||| |||: ||| ||   || :| |  ||:
Db    482 DLTWFQYHSLDVTGFLLACVATVIFIITKC-LFCVWKFVRTGKKGKRD 528


RESULT   5
Q9ESE4
ID   Q9ESE4      PRELIMINARY;      PRT;   527 AA.
AC   Q9ESE4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   OLFACTORY UDP GLUCURONOSYLTRANSFERASE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Heydel J.M.;
RT   "Mus musculus mRNA for olfactory UDP glucuronosyltransferase.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF184901; AAG17003.1; -.
KW   Transferase.
SQ   SEQUENCE   527 AA;  59878 MW;  136FB2A648F39C75 CRC64;


  Query Match             60.9%;  Score 1705.5;  DB 11;  Length 527;
  Best Local Similarity   61.9%;  Pred. No. 1.1e-133;
  Matches  326;  Conservative   70;  Mismatches  110;  Indels   21;  Gaps    5;

Qy     13 LQLFCVGCGFCGKVLVWPCDMSHWLNVKVILEELIVRGHEVTVLTHSKPSLIDYRKPSAL 72
          ||:  :|    | ||:|| : |||||||:|::||: : | ||||  |    |      :|
Db     10 LQISLLGMSLGGNVLIWPMEGSHWLNVKIIIDELLRKEHNVTVLVASGALFITPSISPSL 69

Qy     73 KFEVVHMPQDRTEENEIFVDLALNVL--PGLSTWQSVIK-----LNDFFVEIRGTLKMM 124
           ||:  :|  : :   :  |  |  |  '|  ||  :  |     : :| |   :|:  ||    :
Db     70 TFEIYPVPFGKEKIESVIKDFVLTWLENRPSPSTIWTFYKEMAKVIEEFHLVSRG----I 125

Qy    125 CESFIYNQTLMKKLQETNYDVMLIDPVIPCGDLMAELLAVPFVLTLRISVGGNMERSCGK 184
          |:  : |: || |||:  ::|:| ||| ||||::|  | :||: :|| |    :|: |||
Db    126 CDGVLKNEKLMSKLQKEKFEVLLSDPVFPCGDIVALKLGIPFIYSLRFSPASTVEKHCGK 185

Qy    185 LPAPLSYVPVPMTGLTDRMTFLERVKNSMLSVLFHFWIQDYDYHF----WEEFYSKALGR 240
          :| | ||||  :: |||:|:| :||:|        : :||| :      |: :|:|||||
Db    186 VPFPPSYVPAILSELTDQMSFADRVRN-----FISYRMQDYMFETLWKQWDSYYTKALGR 240

Qy    241 PTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGED 300
          |||||||:|||||||:||||||||:|| |||||||||||||| |||||  |||:|||
Db    241 PTTLCETMGKAEIWLMRTYWDFEFPRPYLPNFEFVGGLHCKPAKPLPKEMEEFVQTSGEH 300

Qy    301 GIVVFSLGSLFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRLYDWIPQNDL 360
          |||||||||: :|:|:||||:|||||||||||||||| | |||:||||:|||||||||
Db    301 GIVVFSLGSMVKNLTDEKANLIASALAQIPQKVLWRYKGKIPDTLGSNTRLFDWIPQNDL 360

Qy    361 LGHPKTKAFITHGGMNGIYEAIYHGVPMVGVPIFGDQLDNIAHMKAKGAAVEINFKTMTS 420
          ||||||:|||||||  ||||||||||:||||||:| || |||||||||||||:|  ||||
Db    361 LGHPKTRAFITHGGTNGIYEAIYHGIPMVGVPMFADQPDNIAHMKAKGAAVEVNMNTMTS 420

Qy    421 EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSAAHD 480
          ||| |||||| : |||||||||||||||||||||||||||||||||||||||||||| ||||
Db    421 SDLLNALRTVINEPSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAAHD 480

Qy    481 LTWFQHYSIDVIGFLLTCVATAIFLFTKCFLFSCQKFNKTRKIEKRE 527
          |:|||::|:||||||| |||:|| |  || ||  ||  |||| :| :
Db    481 LSWFQYHSLDVIGFLLACVASAILLVAKCCLFIFQKVGKTRKKKKSD 527
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Qy     361 LGHPKTKAFITHGGMNGIYEAIYHGVPMVGVPIFGDQLDNIAHMKAKGAAVEINFKTMTS 420
           |||||||:||||||| |||||||||||:||||||:| || |||||||||||||||:|  ||||
Db     361 LGHPKTRAFITHGGTNGIYEAIYHGIPMVGVPMFADQPDNIAHMKAKGAAVEVNMNTMTS 420

Qy     421 EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSAAHD 480
           ||| |:| || :  ||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     421 ADLLSAVRAVINEPFYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAAHD 480

Qy     481 LTWFQHYSIDVIGFLLTCVATAIFLFTKCFLFSCQKFNKTRKIEKRE 527
           |:|||::|:|||||||| |:|:|| |  || ||  ||  || |  ||:
Db     481 LSWFQYHSLDVIGFLLACMASAILLVIKCCLFVFQKIGKTGKKNKRD 527


RESULT   4
A42233
glucuronosyltransferase (EC 2.4.1.17) 2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Jun-1992 #sequence_revision 18-Sep-1992 #text_change 29-Sep-1999
C;Accession: A42233; A24324
R;Mackenzie, P.I.; Rodbourn, L.
J. Biol. Chem. 265, 11328-11332, 1990
A;Title: Organization of the rat UDP-glucuronosyltransferase, UDPGTr-2, gene and charact
A;Reference number: A42233; MUID:90293083
A;Accession: A42233
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-529 <MAC>
A;Cross-references: GB:J05482
A;Note: the authors translated the codon GTA for residue 57 as B, and GTC for residue 11
R;Mackenzie, P.I.
J. Biol. Chem. 261, 6119-6125, 1986
A;Title: Rat liver UDP-glucuronosyltransferase. Sequence and expression of a cDNA encodi
A;Reference number: A24324; MUID:86196018
A;Accession: A24324
A;Molecule type: mRNA
A;Residues: 1-407,'V',409-529 <MA2>
A;Cross-references: GB:M13506; NID:g207580; PIDN:AAA42313.1; PID:g207581
A;Experimental source: liver
C;Superfamily: glucuronosyltransferase
C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein


  Query Match             60.2%;  Score 1687;  DB 2;  Length 529;
  Best Local Similarity   60.0%;  Pred. No. 1.8e-125;
  Matches  316;  Conservative   74;  Mismatches  133;  Indels    4;  Gaps    2;

Qy       3 SDKSALVFLLLQLFC-VGCGFCGKVLVWPCDMSHWLNVKVILEELIVRGHEVTVLTHSKP 61
           | |   ||||:|| |    | |||||||| : |||:|:|:|| ||  ||||||||  |
Db       2 SMKQTSVFLLIQLICYFRPGACGKVLVWPTEYSHWINIKIILNELAQRGHEVTVLVSSAS 61

Qy      62 SLIDYRKPSALKFEVVHMPQDRTEENEIF---VDLALNVLPGLSTWQSVIKLNDFFVEIR 118
            ||:  | |:: ||:  :|  :::    |   :|        || |    |:   | |
Db      62 ILIEPTKESSINFEIYSVPLSKSDLEYSFAKWIDEWTRDFETLSIWTYYSKMQKVFNEYS 121

Qy     119 GTLKMMCESFIYNQTLMKKLQETNYDVMLIDPVIPCGDLMAELLAVPFVLTLRISVGGNM 178
             :: :|:: |:|::|||||| : :||:| | | |||:|:|||  | | :||   |
Db     122 DVVENLCKALIWNKSLMKKLQGSQFDVILADAVGPCGELLAELLKTPLVYSLRFCPGYRC 181

Qy     179 ERSCGKLPAPLSYVPVPMTGLTDRMTFLERVKNSMLSVLFHFWIQDYDYHFWEEFYSKAL 238
           |:  | || | ||||| :: |:||||||:||||| :  : | || | :    | :|||  |
Db     182 EKFSGGLPLPPSYVPVVLSELSDRMTFVERVKNMLQMLYFDFWFQPFKEKSWSQFYSDVL 241

Qy     239 GRPTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSG 298
           |||||| | :|||:||||||:|| ||| |: |||:|||||||||| ||:||| ||||||
Db     242 GRPTTLTEMMGKADIWLIRTFWDLEFPHPFLPNFDFVGGLHCKPAKPLPREMEEFVQSSG 301

Qy     299 EDGIVVFSLGSLFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRLYDWIPQN 358
           | |:|||||||: :|:||||||::|||||||||||:||: |||| |||:||||| |||||
Db     302 EHGVVVFSLGSMVKNLTEEKANVVASALAQIPQKVVWRFDGKKPDTLGSNTRLYKWIPQN 361

Qy     359 DLLGHPKTKAFITHGGMNGIYEAIYHGVPMVGVPIFGDQLDNIAHMKAKGAAVEINFKTM 418
           ||||||||||: ||| |||||||||:|:||:|:| || ||| || |||||| ::|  :
Db     362 DLLGHPKTKAFVAHGGTNGIYEAIYHGIPIVGIPLFADQPDNINHMBAKGAAVRVDFSIL 421

Qy     419 TSEDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSAA 478
           ::  || ||: |: | |||||||||||||||||||||||||||:||||||||||||
Db     422 STTGLLTALKIVMNDPSYKENAMRLSRIHHDQPVKPLDRAVFWIEYVMRHKGAKHLRSTL 481

Qy     479 HDLTWFQHYSIDVIGFLLTCVATAIFLFTKCFLFSCQKFNKTRKIEK 525
           |||:|||::|:|||||| ||   :|: ||  || |:|     | :|
Db     482 HDLSWFQYHSLDVIGFLLLCVVGVVFIITKFCLFCCRKTANMGKKKK 528


RESULT   5
S11309
glucuronosyltransferase (EC 2.4.1.17) - human
N;Alternate names: estriol UDPglucuronosyltransferase
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 29-Sep-1999
C;Accession: S11309
R;Coffman, B.L.; Tephly, T.R.; Irshaid, Y.M.; Green, M.D.; Smith, C.; Jackson, M.R.;
Arch. Biochem. Biophys. 281, 170-175, 1990
A;Title: Characterization and primary sequence of a human hepatic microsomal estriol
A;Reference number: S11309; MUID:90343358
A;Accession: S11309
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-523 <COF>
A;Cross-references: GB:U06641; NID:g458398; PIDN:AAA83406.1; PID:g458399
A;Note: the authors translated the codon AGG for residue 412 as Thr and ACC for resi
C;Superfamily: glucuronosyltransferase
C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein


  Query Match             60.1%;  Score 1684;  DB 2;  Length 523;
  Best Local Similarity   61.7%;  Pred. No. 3e-125;
  Matches  325;  Conservative   72;  Mismatches  118;  Indels   12;  Gaps    5;

Qy       9 VFLLLQLFC-VGCGFCGKVLVWPCDMSHWLNVKVILEELIVRGHEVTVLTHSKPSLIDYR 67
           ||||:|| |    | |||||||| : |||:|:| |||||: |||||||| |  :|::
Db       1 VFLLIQLSCYFSSGSCGKVLVWPTEYSHWINMKTILEELVQRGHEVTVLTSSASTLVNAS 60

Qy      68 KPSALKFEVVHMPQDRTEENEIFVDLALNVLP----GLST---WQSVIKLNDFFVEIRGT 120
           | ||:| ||   |   |:      |  | :|     |:|    |    :| :
Db      61 KSSAIKLEV--YPTSLTK--NYLEDSLLKILDRWIYGVSKNTFWSYFSQLQELCWAYYDY 116

Qy     121 LKMMCESFIYNQTLMKKLQETNYDVMLIDPVIPCGDLMAELLAVPFVLTLRISVGGNMER 180
              :|:  : |: || ||||: :||:  ||| |||:|::||| :|||   ||| |  :|:
Db     117 SNKLCKDAVLNKKLMMKLQESRFDVIPGDPVFPCGELLSELLNIPFVYRSRISRGYTIEK 176

Qy     181 SCGKLPAPLSYVPVPMTGLTDRMTFLERVKNSMLSVLFHFWIQDYDYHFWEEFYSKALGR 240
           : |    | ||||| |: | |:| |:||:|| :  : | || | ||   |::||: |||
Db     177 NGGGFLFPPSYVPVVMSELIDQMIFMERIKNMIHMLYFDFWFQIYDLKKWDQFYSEVLGR 236

Qy     241 PTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGED 300
           |||| ||:|||||:||||||||||:|: || :|||||||||| ||||:| |||||||:
Db     237 PTTLFETMGKAEMWLIRTYWDFEFPRPFLPNVDFVGGLHCKPAKPLPKELEEFVQSSGEN 296

Qy     301 GIVVFSLGSLFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRLYDWIPQNDL 360
           |||||||||:  |::|| ||:|||||||||||||||: ||||:|||:||||| |:|||||
Db     297 GIVVFSLGSMISNMSEESANMIASALAQIPQKVLWRFDGKKPNTLGSNTRLYKWLPQNDL 356

Qy     361 LGHPKTKAFITHGGMNGIYEAIYHGVPMVGVPIFGDQLDNIAHMKAKGAAVEINFKTMTS 420
           |||||||||||||| ||||||||||:||||:|:| || |||||||||||: :: :|||:|
Db     357 LGHPKTKAFITHGGTNGIYEAIYHGIPMVGIPLFADQDDNIAHMKAKGAALSVDIRTMSS 416

Qy     421 EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSAAHD 480
           ||| ||::|| | |||||:|||||||||||||||||||||||||||||||||||||| |||:
Db     417 RDLLNALKSVINDPVYKENAMKLSRIHHDQPMKPLDRAVFWIEFVMRHKGAKHLRVAAHN 476

Qy     481 LTWFQHYSIDVIGFLLTCVATAIFLFTKCFLFSCQKFNKTRKIEKRE 527
           ||| |::|:||| |||  ||| || :|  |  | :||:
Db     477 LTWIQYHSLDVIAFLLAWVATVIFIITKFCLFCFRKLAKKGKKKKRD 523


RESULT   6
```